



Blast 2 Sequences results

PubMed

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BLAST

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Taxonomy

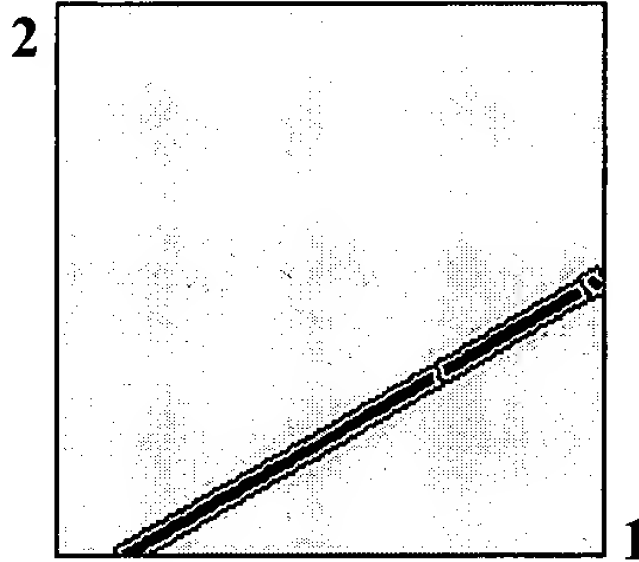
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

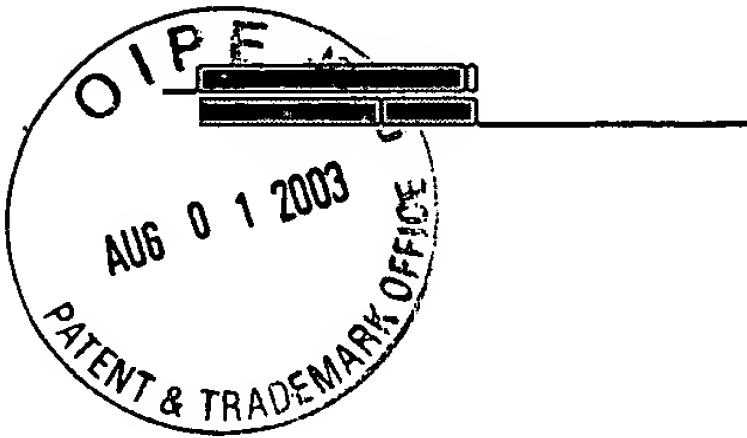
Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ Align

Sequence 1 lcl|seq_1 Length 666 (1 .. 666)

Sequence 2 lcl|seq_2 Length 1162 (1 .. 1162)



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NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 987 bits (2552), Expect = 0.0

Identities = 498/589 (84%), Positives = 511/589 (86%), Gaps = 2/589 (0%)

Query: 79 MVAIADARYDTSNDNSLIDTVAKYSVDDGETWETQIAIKNXXXXXXXXXXDPTVIVKGNK 138
MVAIADARY+TS++NSLIDTVAKYSVDDGETWETQIAIKN DPTVIVKGNK
Sbjct: 1 MVAIADARYETSSNSLIDTVAKYSVDDGETWETQIAIKNSRVSSVSRVVDPTVIVKGNK 60

Query: 139 LYVLVGXXXXXXXXXXXXHGDARDWDILLAVGEVTKSTAGGKITASIKWGSPVSLKKFFPA 198
LYVLVG HGDARDWDILLAVGEVTKSTAGGKITASIKWGSPVSLKKFFPA
Sbjct: 61 LYVLVGSYYSSRSYWSSHGDARDWDILLAVGEVTKSTAGGKITASIKWGSPVSLKKFFPA 120

Query: 199 EMEGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKKKQVFSKIFYSEDDGKTWKFGKGRSD 258
EMEGMHTNQFLGGAGVAIVASNGNLVYPVQVTN+KQVFSKIFYSEDDGKTWKFGKGRSD
Sbjct: 121 EMEGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKRKQVFSKIFYSEDDGKTWKFGKGRSD 180

Query: 259 FGCSEPVALEWEGKLIINTRVDWKRRLVYESSDMEKPWVEAVGTVSRVWGSPSPKSNQPGS 318
FGCSEPVALEWEGKLIINTRVDWKRRLVYESSDMEKPWVEAVGTVSRVWGSPSPKSNQPGS
Sbjct: 181 FGCSEPVALEWEGKLIINTRVDWKRRLVYESSDMEKPWVEAVGTVSRVWGSPSPKSNQPGS 240

Query: 319 QSSFTAVTIEGMRVMLFTHPLNFKGRWLRDRLNLWLTDNQRIYNVGQVSIQDENSAYSSV 378
Q+SFTAVTIEGMRVMLFTHPLNFKGR +RDRLNLWLTDNQRIYNVGQVSIQDENSAYSSV
Sbjct: 241 QTSFTAVTIEGMRVMLFTHPLNFKGRCVRDRLNLWLTDNQRIYNVGQVSIQDENSAYSSV 300

Query: 379 LYKDDKLYCLHEINTDEVYSLVFARLVGELRIIKSVLRSWKNWDSHLSSICTPADPAASS 438
LYKDDKLYCLHEINTDEVYSLVFARLVGELRIIKSVLRSWKNW + +
Sbjct: 301 LYKDDKLYCLHEINTDEVYSLVFARLVGELRIIKSVLRSWKNWTATCPAFAPLLIQPLRR 360

Query: 439 SESGCGPAVTTVGLVGLSGNASQNVWEDAYRCVNASTANAERVRNGLKFAGVGGGALWP 498
P + L+ F + + +YRCVNASTANAERVRNGLKFAGVGGGALWP

EXHIBIT

Sbjct: 361 QRVVVVPLSPRLVLLAFCRQRLPKRM-GGSYRCVNASTANAERVRNGLKFAGVGGGALWP 419

Query: 499 VSQQGQNQRYRFANHAFTLVASVTIHEAPRAASXXXXXXXXXXXXXXXXXXXXYDEKHQWQ 558
VSQQGQNQRYRFANHAFTLVASVTIHEAPRAAS YDEKHQWQ

Sbjct: 420 VSQQGQNQRYRFANHAFTLVASVTIHEAPRAASPLLGASLDSSGGKKLLGLSYDEKHQWQ 479

Query: 559 PIYGSTPVTPTGSWETGKRYHLVLTMANKIGSVYIDGELLEGGSGQTVVPDGRTPDISHFY 618
PIYGSTPVTPTGSWETGKRYHLVLTMANKIGSVYIDGELLEGGSGQTVVPDGRTPDISHFY

Sbjct: 480 PIYGSTPVTPTGSWETGKRYHLVLTMANKIGSVYIDGELLEGGSGQTVVPDGRTPDISHFY 539

Query: 619 VGGYKRSDMPTISHVTVNNVLLYN-RQLNTEEIRTLFLSQDLIGTEAHM 666
VGGYKRSDMPTISHVTVNNVLLYN RQLNTEEIRTLFLSQDLIGTEAHM

Sbjct: 540 VGGYKRSDMPTISHVTVNNVLLYNRRQLNTEEIRTLFLSQDLIGTEAHM 588

CPU time: 0.17 user secs. 0.07 sys. secs 0.24 total secs.

Lambda	K	H
0.317	0.134	0.406

Gapped Lambda	K	H
0.267	0.0410	0.140

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Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 105,870
Number of Sequences: 0
Number of extensions: 556
Number of successful extensions: 5
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 666
length of database: 463,592,631
effective HSP length: 134
effective length of query: 532
effective length of database: 463,592,497
effective search space: 246631208404
effective search space used: 246631208404
T: 9
A: 40
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 78 (34.7 bits)